

48231A\_pctus\_SEQLIST.ST25  
SEQUENCE LISTING

<110> Greenwald, Iva  
Levitan, Diane

<120> IDENTIFICATION OF SEL 12 AND USES THEREOF

<130> 0575/48231-A-PCT-US

<140> 09/043,944

<141> 1998-03-27

<150> PCT/US96/15727

<151> 1996-09-27

<150> 60/004,387

<151> 1995-09-27

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 461

<212> PRT

<213> C. elegans

<220>

<221> misc\_feature

<223> Fig. 1A

<400> 1

## 48231A\_pctus\_SEQLIST.ST25

Met Pro Ser Thr Arg Arg Gln Gln Glu Gly Gly Gly Ala Asp Ala Glu  
 1 5 10 15  
 Thr His Thr Val Tyr Gly Thr Asn Leu Ile Thr Asn Arg Asn Ser Gln  
 20 25 30  
 Glu Asp Glu Asn Val Val Glu Glu Ala Glu Leu Lys Tyr Gly Ala Ser  
 35 40 45  
 His Val Ile His Leu Phe Val Pro Val Ser Leu Cys Met Ala Leu Val  
 50 55 60  
 Val Phe Thr Met Asn Thr Ile Thr Phe Tyr Ser Gln Asn Asn Gly Arg  
 65 70 75 80  
 His Leu Leu Ser His Pro Phe Val Arg Glu Thr Asp Ser Ile Val Glu  
 85 90 95  
 Lys Gly Leu Met Ser Leu Gly Asn Ala Leu Val Met Leu Cys Val Val  
 100 105 110  
 Val Leu Met Thr Val Leu Leu Ile Val Phe Tyr Lys Tyr Lys Phe Tyr  
 115 120 125  
 Lys Leu Ile His Gly Trp Leu Ile Val Ser Ser Phe Leu Leu Leu Phe  
 130 135 140  
 Leu Phe Thr Thr Ile Tyr Val Gln Glu Val Leu Lys Ser Phe Asp Val  
 145 150 155 160  
 Ser Pro Ser Ala Leu Leu Val Leu Phe Gly Leu Gly Asn Tyr Gly Val  
 165 170 175  
 Leu Gly Met Met Cys Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln  
 180 185 190  
 Phe Tyr Leu Ile Thr Met Ser Ala Leu Met Ala Leu Val Phe Ile Lys  
 195 200 205  
 Tyr Leu Pro Glu Trp Thr Val Trp Phe Val Leu Phe Val Ile Ser Val  
 210 215 220  
 Trp Asp Leu Val Ala Val Leu Thr Pro Lys Gly Pro Leu Arg Tyr Leu  
 225 230 235 240  
 Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile Phe Pro Ala Leu Ile  
 245 250 255

48231A\_pctus\_SEQLIST.ST25

Tyr Ser Ser Gly Val Ile Tyr Pro Tyr Val Leu Val Thr Ala Val Glu  
 260 265 270  
 Asn Thr Thr Asp Pro Arg Glu Pro Thr Ser Ser Asp Ser Asn Thr Ser  
 275 280 285  
 Thr Ala Phe Pro Gly Glu Ala Ser Cys Ser Ser Glu Thr Pro Lys Arg  
 290 295 300  
 Pro Lys Val Lys Arg Ile Pro Gln Lys Val Gln Ile Glu Ser Asn Thr  
 305 310 315 320  
 Thr Ala Ser Thr Thr Gln Asn Ser Gly Val Arg Val Glu Arg Glu Leu  
 325 330 335  
 Ala Ala Glu Arg Pro Thr Val Gln Asp Ala Asn Phe His Arg His Glu  
 340 345 350  
 Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile Phe Tyr  
 355 360 365  
 Ser Val Leu Leu Gly Lys Ala Ser Ser Tyr Phe Asp Trp Asn Thr Thr  
 370 375 380  
 Ile Ala Cys Tyr Val Ala Ile Leu Ile Gly Leu Cys Phe Thr Leu Val  
 385 390 395 400  
 Leu Leu Ala Val Phe Lys Arg Ala Leu Pro Ala Leu Gln Phe Pro Phe  
 405 410 415  
 Ser Pro Asp Ser Phe Phe Thr Phe Val Pro Ala Gly Ser Ser Pro His  
 420 425 430  
 Leu Leu His Lys Ser Leu Lys Ser Val Tyr Tyr Ile Asn Ser Leu Phe  
 435 440 445  
 Leu Pro Phe Leu Cys Ile Ile Asn Phe Ser Ile Ile Ser  
 450 455 460

<210> 2

<211> 467

<212> PRT

<213> human

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Fig. 2A S182

&lt;400&gt; 2

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met  
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn  
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu  
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu  
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys  
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val  
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln  
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg  
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val  
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys  
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe  
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala  
180 185 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val  
195 200 205

## 48231A\_pctus\_SEQLIST.ST25

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
 210 215 220  
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 225 230 235 240  
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 245 250 255  
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 260 265 270  
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
 275 280 285  
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 290 295 300  
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr  
 305 310 315 320  
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe  
 325 330 335  
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
 340 345 350  
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile  
 355 360 365  
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
 370 375 380  
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
 385 390 395 400  
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
 405 410 415  
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
 420 425 430  
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
 435 440 445  
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln  
 450 455 460

48231A\_pctus\_SEQLIST.ST25

Phe Tyr Ile  
465

<210> 3

<211> 157

<212> PRT

<213> C. elegans

<220>

<221> MISC\_FEATURE

<222> (11)..(11)

<223> unknown amino acid

<400> 3

Glu Gly Lys Ser Pro Ser Asn Thr Glu Arg Xaa Val Ile Met Leu Phe  
1 5 10 15

Val Pro Val Thr Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser  
20 25 30

Val Arg Phe Tyr Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe  
35 40 45

Thr Glu Asp Thr Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu  
50 55 60

Asn Thr Leu Ile Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu  
65 70 75 80

Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu  
85 90 95

Ile Met Ser Ser Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu  
100 105 110

Gly Glu Val Leu Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu  
115 120 125

Leu Leu Thr Val Trp Glu Leu Arg Gly Ser Gly His Gly Val His Pro  
130 135 140

## 48231A\_pctus\_SEQLIST.ST25

Leu Glu Gly Ala Phe Gly Ala Ala Glu Ala Tyr Leu Ser  
 145 150 155

<210> 4

<211> 465

<212> PRT

<213> C. elegans

<220>

<221> misc\_feature

<223> Fig. 2A SPE-4

<400> 4

Met Asp Thr Leu Arg Ser Ile Ser Ser Glu Leu Val Arg Ser Ser Gln  
 1 5 10 15

Leu Arg Trp Thr Leu Phe Ser Val Ile Ala Asn Met Ser Leu Thr Leu  
 20 25 30

Ser Ile Trp Ile Gly Val Tyr Asn Met Glu Val Asn Ser Glu Leu Ser  
 35 40 45

Lys Thr Tyr Phe Leu Asp Pro Ser Phe Glu Gln Thr Thr Gly Asn Leu  
 50 55 60

Leu Leu Asp Gly Phe Ile Asn Gly Val Gly Thr Ile Leu Val Leu Gly  
 65 70 75 80

Cys Val Ser Phe Ile Met Leu Ala Phe Val Leu Phe Asp Phe Arg Arg  
 85 90 95

Ile Val Lys Ala Trp Leu Thr Leu Ser Cys Leu Leu Ile Leu Phe Gly  
 100 105 110

Val Ser Ala Gln Thr Leu His Asp Met Phe Ser Gln Val Phe Asp Gln  
 115 120 125

Asp Asp Asn Asn Gln Tyr Tyr Met Thr Ile Val Leu Ile Val Val Pro  
 130 135 140

Thr Val Val Tyr Gly Phe Gly Gly Ile Tyr Ala Phe Phe Ser Asn Ser  
 145 150 155 160

## 48231A\_pctus\_SEQLIST.ST25

Ser Leu Ile Leu His Gln Ile Phe Val Val Thr Asn Cys Ser Leu Ile  
 165 170 175  
 Ser Val Phe Tyr Leu Arg Val Phe Pro Ser Lys Thr Thr Trp Phe Val  
 180 185 190  
 Leu Trp Ile Val Leu Phe Trp Asp Leu Phe Ala Val Leu Ala Pro Met  
 195 200 205  
 Gly Pro Leu Lys Lys Val Gln Glu Lys Ala Ser Asp Tyr Ser Lys Cys  
 210 215 220  
 Val Leu Asn Leu Ile Met Phe Ser Ala Asn Glu Lys Arg Leu Thr Ala  
 225 230 235 240  
 Gly Ser Asn Gln Glu Glu Thr Asn Glu Gly Glu Glu Ser Thr Ile Arg  
 245 250 255  
 Arg Thr Val Lys Gln Thr Ile Glu Tyr Tyr Thr Lys Arg Glu Ala Gln  
 260 265 270  
 Asp Asp Glu Phe Tyr Gln Lys Ile Arg Gln Arg Arg Ala Ala Ile Asn  
 275 280 285  
 Pro Asp Ser Val Pro Thr Glu His Ser Pro Leu Val Glu Ala Glu Pro  
 290 295 300  
 Ser Pro Ile Glu Leu Lys Glu Lys Asn Ser Thr Glu Glu Leu Ser Asp  
 305 310 315 320  
 Asp Glu Ser Asp Thr Ser Glu Thr Ser Ser Gly Ser Ser Asn Leu Ser  
 325 330 335  
 Ser Ser Asp Ser Ser Thr Thr Val Ser Thr Ser Asp Ile Ser Thr Ala  
 340 345 350  
 Glu Glu Cys Asp Gln Lys Glu Trp Asp Asp Leu Val Ser Asn Ser Leu  
 355 360 365  
 Pro Asn Asn Asp Lys Arg Pro Ala Thr Ala Ala Asp Ala Leu Asn Asp  
 370 375 380  
 Gly Glu Val Leu Arg Leu Gly Phe Gly Asp Phe Val Phe Tyr Ser Leu  
 385 390 395 400  
 Leu Ile Gly Gln Ala Ala Ala Ser Gly Cys Pro Phe Ala Val Ile Ser  
 405 410 415



48231A\_pctus\_SEQLIST.ST25

Ala Ala Leu Gly Ile Leu Phe Gly Leu Val Val Thr Leu Thr Val Phe  
420 425 430

Ser Thr Glu Glu Ser Thr Thr Pro Ala Leu Pro Leu Pro Val Ile Cys  
435 440 445

Gly Thr Phe Cys Tyr Phe Ser Ser Met Phe Phe Trp Glu Gln Leu Tyr  
450 455 460

Gly  
465

<210> 5

<211> 1500

<212> DNA

<213> C. elegans

<220>

<221> misc\_feature

<223> Fig. 1A

<400> 5

gtttaattac ccaagtttga gatgccttcc acaaggagac aacaggaggg cggaggtgca	60
gatgcggaaa cacataccgt ttacggtaca aatctgataa caaatcggaa tagccaagaa	120
gacgaaaatg ttgtggaaga agcggagctg aaatacggag catctcacgt tattcatcta	180
tttgtgccgg tgctactatg catggctctg gttgttttta cgatgaacac gattacgttt	240
tatagtcaaa acaatggaag gcatttacta tcacatcctt ttgtccggga aacagacagt	300
atcgttgaga agggattgat gtcacttggg aatgctctcg tcatgttgtg cgtggtcggt	360
ctgatgacag ttctgctgat tgttttctat aaatacaagt ttataagct tattcatgga	420
tggcttattg tcagcagttt tcttcttctt ttcctattca ctacaatcta tgtgcaagaa	480
gttctgaaaa gtttcgatgt gtctcccagc gcactattgg tttgttttg actgggtaac	540
tatggagttc tcggaatgat gtgtatacat tggaaaggtc cattgcgtct gcaacagttc	600
taccttatta caatgtctgc actaatggct ctgggtcttta tcaagtacct accagaatgg	660
actgtgtggt ttgtgctggt tggtatctcg gtttgggatc tggttgccgt gctcacacca	720
aaaggaccat tgagatatat ggtggaaact gcacaggaga gaaacgagcc aattttccc	780

## 48231A\_pctus\_SEQLIST.ST25

```

gcgctgattt attcgtctgg agtcatctat ccctacgttc ttgttactgc agttgaaaac      840
acgacagacc cccgtgaacc gacgtcgtca gactcaaata cttctacagc ttttcctgga      900
gaggcgagtt gttcatctga aacgccaaaa cggccaaaag tgaaacgaat tcctcaaaaa      960
gtgcaaactc aatcgaatac tacagcttca acgacacaaa actctggagt aagggtggaa     1020
cgggagctag ctgctgagag accaactgta caagacgcca attttcacag gcacgaagag     1080
gaagagagag gtgtgaaact tggctctgggc gacttcattt tctactctgt tctcctcggc     1140
aaggcttcat cgtactttga ctggaacacg actatcgctt gttatgtggc cattcttattc     1200
ggctctctgt tctactctgt cctgctcgcc gtcttcaaac gagcactccc ggctctgcaa     1260
tttccatttt ctccggactc attttttact tttgtaccgc ctggatcatc accccatttg     1320
ttacacaagt ctctcaaaag tgtttattat attaatcttc tgtttttgcc atttctttgc     1380
atcatcaact tttcgattat atcttgagcg atctcaaagc tttattttac atacctattt     1440
atttttgaac tttgtcattt aagttatata aataatttat taaaaaaaaa aaaaaaaaaa     1500

```

&lt;210&gt; 6

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; C. elegans

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Fig. 2A sel-12

&lt;400&gt; 6

```

Met Pro Ser Thr Arg Arg Gln Gln Glu Gly Gly Gly Ala Asp Ala Glu
1           5           10           15

```

```

Thr His Thr Val Tyr Gly Thr Asn Leu Ile Thr Asn Arg Asn Ser Gln
20           25           30

```

```

Glu Asp Glu Asn Val Val Glu Glu Ala Glu Leu Lys Tyr Gly Ala Ser
35           40           45

```

```

His Val Ile His Leu Phe Val Pro Val Ser Leu Cys Met Ala Leu Val
50           55           60

```

```

Val Phe Thr Met Asn Thr Ile Thr Phe Tyr Ser Gln Asn Asn Gly Arg
65           70           75           80

```

48231A\_pctus\_SEQLIST.ST25

His Leu Leu Ser His Pro Phe Val Arg Glu Thr Asp Ser Ile Val Glu  
85 90 95

Lys Gly Leu Met Ser Leu Gly Asn Ala Leu Val Met Leu Cys Val Val  
100 105 110

Val Leu Met Thr Val Leu Leu Ile Val Phe Tyr Lys Tyr Lys Phe Tyr  
115 120 125

Lys Leu Ile His Gly Trp Leu Ile Val Ser Ser Phe Leu Leu Leu Phe  
130 135 140

Leu Phe Thr Thr Ile Tyr Val Gln Glu Val Leu Lys Ser Phe Asp Val  
145 150 155 160

Ser Pro Ser Ala Leu Leu Val Leu Phe Gly Leu Gly Asn Tyr Gly Val  
165 170 175

Leu Gly Met Met Cys Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln  
180 185 190

Phe Tyr Leu Ile Thr Met Ser Ala Leu Met Ala Leu Val Phe Ile Lys  
195 200 205

Tyr Leu Pro Glu Trp Thr Val Trp Phe Val Leu Phe Val Ile Ser Val  
210 215 220

Trp Asp Leu Val Ala Val Leu Thr Pro Lys Gly Pro Leu Arg Tyr Leu  
225 230 235 240

Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile Phe Pro Ala Leu Ile  
245 250 255

Tyr Ser Ser Gly Val Ile Tyr Pro Tyr Val Leu Val Thr Ala Val Glu  
260 265 270

Asn Thr Thr Asp Pro Arg Glu Pro Thr Ser Ser Asp Ser Asn Thr Ser  
275 280 285

Thr Ala Phe Pro Gly Glu Ala Ser Cys Ser Ser Glu Thr Pro Lys Arg  
290 295 300

Pro Lys Val Lys Arg Ile Pro Gln Lys Val Gln Ile Glu Ser Asn Thr  
305 310 315 320

Thr Ala Ser Thr Thr Gln Asn Ser Gly Val Arg Val Glu Arg Glu Leu  
Page 11

Ala Ala Glu Arg Pro Thr Val Gln Asp Ala Asn Phe His Arg His Glu  
340 345 350

Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile Phe Tyr  
355 360 365

Ser Val Leu Leu Gly Lys Ala Ser Ser Tyr Phe Asp Trp Asn Thr Thr  
370 375 380

Ile Ala Cys Tyr Val Ala Ile Leu Ile Gly Leu Cys Phe Thr Leu Val  
385 390 395 400

Leu Leu Ala Val Phe Lys Arg Ala Leu Pro Ala Leu Gln Phe Pro Phe  
405 410 415

Ser Pro Asp Ser Phe Phe Thr Phe Val Pro Ala Gly Ser Ser Pro His  
420 425 430

Leu Leu His Lys Ser Leu Lys Ser Val Tyr Tyr Ile Asn Ser Leu Phe  
435 440 445

Leu Pro Phe Leu Cys Ile Ile Asn Phe Ser Ile Ile Ser  
450 455 460

<210> 7

<211> 21

<212> DNA

<213> C. elegans

<220>

<221> artificial\_sequence

<222> (1)..(21)

<223> primer or probe

<400> 7

tgtctgagtt actagtttttc c

21

<210> 8

<211> 24

<212> DNA

<213> C. elegans

<220>

<221> artificial\_sequence

<222> (1)..(24)

<223> primer or probe

<400> 8

ggaatctgaa gcacctgtaa gcat

24

<210> 9

<211> 448

<212> PRT

<213> human

<220>

<221> misc\_feature

<223> Fig. 2A E5-1

<220>

<221> misc\_feature

<223> Fig. 2A E5-1/STM2

<400> 9

Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu  
1 5 10 15

Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln  
20 25 30

Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg  
35 40 45

Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val  
50 55 60

## 48231A\_pctus\_SEQLIST.ST25

Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr  
 65 70 75 80  
 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr  
 85 90 95  
 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr  
 100 105 110  
 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr  
 115 120 125  
 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile  
 130 135 140  
 Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr  
 145 150 155 160  
 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser  
 165 170 175  
 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu  
 180 185 190  
 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val  
 195 200 205  
 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro  
 210 215 220  
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala  
 225 230 235 240  
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu  
 245 250 255  
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly  
 260 265 270  
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile  
 275 280 285  
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met  
 290 295 300  
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp  
 305 310 315 320

48231A\_pctus\_SEQLIST.ST25

Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr  
325 330 335

Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu  
340 345 350

Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile  
355 360 365

Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp  
370 375 380

Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys  
385 390 395 400

Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu  
405 410 415

Pro Ile Ser Thr Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn  
420 425 430

Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile  
435 440 445

<210> 10

<211> 27

<212> DNA

<213> human

<220>

<221> artifical\_sequence

<222> (1)..(27)

<223> sense primer for human PS1; pg 52

<400> 10

gggggtaccat gacagagtta cctgcac

27

<210> 11

<211> 25

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(25)

<223> antisense primer for human PS1; pg. 52

<400> 11

ccgggatcca tgggattcta accgc

25

<210> 12

<211> 27

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(27)

<223> PS1 M146L sense primer 1

<400> 12

gtcattgttg tcctgactat cctcctg

27

<210> 13

<211> 20

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(20)

<223> PS1 M146L antisense primer 1



<400> 13  
gaggagtaaa tgagagctgg 20

<210> 14

<211> 27

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(27)

<223> PS1 M146L sense primer 2

<400> 14  
caggaggata gtcaggacaa caatgac 27

<210> 15

<211> 19

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(19)

<223> PS1 M146L antisense primer 2

<400> 15  
caggtggtgg agcaagatg 19

<210> 16

<211> 20

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(20)

<223> PS1 H163R primer

<400> 16  
ctaggtcatc cgtgcctggc

20

<210> 17

<211> 20

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(20)

<223> PS1 H163R primer

<400> 17  
gccaggcacg gatgacctag

20

<210> 18

<211> 26

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(26)

<223> PS1 L286V primer

<400> 18  
cgctttttcc agctgtcatt tactcc

26

<210> 19

<211> 27

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(27)

<223> PS1 L286V primer

<400> 19

ccggaattct caggttgtgt tccagtc

27

<210> 20

<211> 26

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(26)

<223> PS1 L286V primer

<400> 20

ggagtaaattg acagctggaa aaagcg

26

<210> 21

<211> 24

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(24)

<223> PS1 L286V primer

<400> 21  
ggatccattg ttgtcatgac tatc 24

<210> 22

<211> 23

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(23)

<223> PS1 C410Y primer

<400> 22  
caaccatagc ctatttcgta gcc 23

<210> 23

<211> 33

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(33)

<223> PS1 C410Y primer

<400> 23  
gccagtgaat tgtaatacga ctactatag ggc 33

<210> 24

<211> 23

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(23)

<223> PS1 C410Y primer

<400> 24

ggctacgaaa taggctatgg ttg

23

<210> 25

<211> 24

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(24)

<223> PS1 C410Y primer

<400> 25

ccggaattct gaatggactg cgtg

24

<210> 26

<211> 27

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(27)

<223> PS2 primer

<400> 26

ccggtaccaa gtgttcgtgg tgcttcc

27

48231A\_pctus\_SEQLIST.ST25

<210> 27

<211> 29

<212> DNA

<213> human

<220>

<221> artificial\_sequence

<222> (1)..(29)

<223> PS2 primer

<400> 27

ccgtctagac ctcagatgta gagctgatg

29